

## SEQUENCE LISTING

<110> Institut Pasteur  
Roche Diagnostics GmbH  
Pharma-Waldhof GmbH & Co.KG

<120> Enzymatic synthesis of deoxyribonucleosides

<130> 20373PWO Deoxyribonucleosides

<140>

<141>

)<150> EP99116425.2

<151> 1999-08-20

<160> 20

<170> PatentIn Ver. 2.1

<210> 1

<211> 1323

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1320)

<400> 1

ttg ttt ctc gca caa gaa att att cgt aaa aaa cgt gat ggt cat gcg 48  
Leu Phe Leu Ala Gln Glu Ile Ile Arg Lys Lys Arg Asp Gly His Ala  
1 5 10 15

ctg agc gat gaa gaa att cgt ttc ttt atc aac ggt att cgc gac aac 96  
Leu Ser Asp Glu Glu Ile Arg Phe Phe Ile Asn Gly Ile Arg Asp Asn  
20 25 30

act atc tcc gaa ggg cag att gcc gcc ctc gcg atg acc att ttc ttc 144  
Thr Ile Ser Glu Gly Gln Ile Ala Ala Leu Ala Met Thr Ile Phe Phe  
35 40 45

2/36

cac gat atg aca atg cct gag cgt gtc tcg ctg acc atg gcg atg cga 192  
 His Asp Met Thr Met Pro Glu Arg Val Ser Leu Thr Met Ala Met Arg  
 50 55 60

gat tca gga acc gtt ctc gac tgg aaa agc ctg cat ctg aat ggc ccg 240  
 Asp Ser Gly Thr Val Leu Asp Trp Lys Ser Leu His Leu Asn Gly Pro  
 65 70 75 80

att gtt gat aaa cac tcc acc ggt ggc gtc ggc gat gtg act tcg ctg 288  
 Ile Val Asp Lys His Ser Thr Gly Gly Val Gly Asp Val Thr Ser Leu  
 85 90 95

atg ttg ggg ccg atg gtc gca gcc tgc ggc tat att ccg atg atc 336  
 Met Leu Gly Pro Met Val Ala Ala Cys Gly Gly Tyr Ile Pro Met Ile  
 100 105 110

tct ggt cgc ggc ctc ggt cat act ggc ggt acg ctc gac aaa ctg gaa 384  
 Ser Gly Arg Gly Leu Gly His Thr Gly Gly Thr Leu Asp Lys Leu Glu  
 115 120 125

tcc atc cct ggc ttc gac att ttc ccg gat gac aac cgt ttc cgc gaa 432  
 Ser Ile Pro Gly Phe Asp Ile Phe Pro Asp Asn Arg Phe Arg Glu  
 130 135 140

att att aaa gac gtc ggc gtg gcg att atc ggt cag acc agt tca ctg 480  
 Ile Ile Lys Asp Val Gly Val Ala Ile Ile Gly Gln Thr Ser Ser Leu  
 145 150 155 160

gct ccg gct gat aaa cgt ttc tac gcg acc cgt gat att acc gca acc 528  
 Ala Pro Ala Asp Lys Arg Phe Tyr Ala Thr Arg Asp Ile Thr Ala Thr  
 165 170 175

gtg gac tcc atc ccg ctg atc acc gcc tct att ctg gcg aag aaa ctt 576  
 Val Asp Ser Ile Pro Leu Ile Thr Ala Ser Ile Leu Ala Lys Lys Leu  
 180 185 190

gcg gaa ggt ctg gac gcg ctg gtg atg gac gtg aaa gtg ggt agc ggc 624  
 Ala Glu Gly Leu Asp Ala Leu Val Met Asp Val Lys Val Gly Ser Gly  
 195 200 205

gcg ttt atg ccg acc tac gaa ctc tct gaa gcc ctt gcc gaa gcg att 672  
 Ala Phe Met Pro Thr Tyr Glu Leu Ser Glu Ala Leu Ala Glu Ala Ile  
 210 215 220

3/36

gtt ggc gtg gct aac ggc gct ggc gtg cgc acc acc gcg ctg ctc acc	720
Val Gly Val Ala Asn Gly Ala Gly Val Arg Thr Thr Ala Leu Leu Thr	
225 230 235 240	
gac atg aat cag gta ctg gcc tcc agt gca ggt aac gcg gtt gaa gtt	768
Asp Met Asn Gln Val Leu Ala Ser Ser Ala Gly Asn Ala Val Glu Val	
245 250 255	
cgt gaa gcg gtg cag ttc ctg acg ggt gaa tat cgt aac ccg cgt ctg	816
Arg Glu Ala Val Gln Phe Leu Thr Gly Glu Tyr Arg Asn Pro Arg Leu	
260 265 270	
ttt gat gtc acg atg gcg ctg tgc gtg gag atg ctg atc tcc ggc aaa	864
Phe Asp Val Thr Met Ala Leu Cys Val Glu Met Leu Ile Ser Gly Lys	
275 280 285	
ctg gcg aaa gat gac gcc gaa gcg cgc gcg aaa ttg cag gcg gtg ctg	912
Leu Ala Lys Asp Asp Ala Glu Ala Arg Ala Lys Leu Gln Ala Val Leu	
290 295 300	
gac aac ggt aaa gcg gca gaa gtc ttt ggt cgt atg gta gcg gca caa	960
Asp Asn Gly Lys Ala Ala Glu Val Phe Gly Arg Met Val Ala Ala Gln	
305 310 315 320	
aaa ggc ccg acc gac ttc gtt gag aac tac gcg aag tat ctg ccg aca	1008
Lys Gly Pro Thr Asp Phe Val Glu Asn Tyr Ala Lys Tyr Leu Pro Thr	
325 330 335	
gcg atg ctg acg aaa gca gtc tat gct gat acc gaa ggt ttt gtc agt	1056
Ala Met Leu Thr Lys Ala Val Tyr Ala Asp Thr Glu Gly Phe Val Ser	
340 345 350	
gaa atg gat acc cgc gcg ctg ggg atg gca gtg gtt gca atg ggc ggc	1104
Glu Met Asp Thr Arg Ala Leu Gly Met Ala Val Val Ala Met Gly Gly	
355 360 365	
gga cgc cgt cag gca tct gac acc atc gat tac agc gtc ggc ttt act	1152
Gly Arg Arg Gln Ala Ser Asp Thr Ile Asp Tyr Ser Val Gly Phe Thr	
370 375 380	
gat atg gcg cgt ctg ggc gac cag gta gac ggt cag cgt ccg ctg gcg	1200
Asp Met Ala Arg Leu Gly Asp Gln Val Asp Gly Gln Arg Pro Leu Ala	
385 390 395 400	

4/36

gtt atc cac gcg aaa gac gaa aac aac tgg cag gaa gcg gcg aaa gcg 1248  
 Val Ile His Ala Lys Asp Glu Asn Asn Trp Gln Glu Ala Ala Lys Ala  
 405 410 415

gtg aaa gcg gca att aaa ctt gcc gat aaa gca ccg gaa agc aca cca 1296  
 Val Lys Ala Ala Ile Lys Leu Ala Asp Lys Ala Pro Glu Ser Thr Pro  
 420 425 430

act gtc tat cgc cgt atc agc gaa taa 1323  
 Thr Val Tyr Arg Arg Ile Ser Glu  
 435 440

<210> 2  
 <211> 440  
 <212> PRT  
 <213> Escherichia coli

<400> 2  
 Leu Phe Leu Ala Gln Glu Ile Ile Arg Lys Lys Arg Asp Gly His Ala  
 1 5 10 15

Leu Ser Asp Glu Glu Ile Arg Phe Phe Ile Asn Gly Ile Arg Asp Asn  
 20 25 30

Thr Ile Ser Glu Gly Gln Ile Ala Ala Leu Ala Met Thr Ile Phe Phe  
 35 40 45

His Asp Met Thr Met Pro Glu Arg Val Ser Leu Thr Met Ala Met Arg  
 50 55 60

Asp Ser Gly Thr Val Leu Asp Trp Lys Ser Leu His Leu Asn Gly Pro  
 65 70 75 80

Ile Val Asp Lys His Ser Thr Gly Val Gly Asp Val Thr Ser Leu  
 85 90 95

Met Leu Gly Pro Met Val Ala Ala Cys Gly Gly Tyr Ile Pro Met Ile  
 100 105 110

Ser Gly Arg Gly Leu Gly His Thr Gly Gly Thr Leu Asp Lys Leu Glu  
 115 120 125

Ser Ile Pro Gly Phe Asp Ile Phe Pro Asp Asn Arg Phe Arg Glu  
 130 135 140

5/36

Ile Ile Lys Asp Val Gly Val Ala Ile Ile Gly Gln Thr Ser Ser Leu  
145 150 155 160

Ala Pro Ala Asp Lys Arg Phe Tyr Ala Thr Arg Asp Ile Thr Ala Thr  
165 170 175

Val Asp Ser Ile Pro Leu Ile Thr Ala Ser Ile Leu Ala Lys Lys Leu  
180 185 190

Ala Glu Gly Leu Asp Ala Leu Val Met Asp Val Lys Val Gly Ser Gly  
195 200 205

Ala Phe Met Pro Thr Tyr Glu Leu Ser Glu Ala Leu Ala Glu Ala Ile  
210 215 220

Val Gly Val Ala Asn Gly Ala Gly Val Arg Thr Thr Ala Leu Leu Thr  
225 230 235 240

Asp Met Asn Gln Val Leu Ala Ser Ser Ala Gly Asn Ala Val Glu Val  
245 250 255

Arg Glu Ala Val Gln Phe Leu Thr Gly Glu Tyr Arg Asn Pro Arg Leu  
260 265 270

Phe Asp Val Thr Met Ala Leu Cys Val Glu Met Leu Ile Ser Gly Lys  
275 280 285

Leu Ala Lys Asp Asp Ala Glu Ala Arg Ala Lys Leu Gln Ala Val Leu  
290 295 300

Asp Asn Gly Lys Ala Ala Glu Val Phe Gly Arg Met Val Ala Ala Gln  
305 310 315 320

Lys Gly Pro Thr Asp Phe Val Glu Asn Tyr Ala Lys Tyr Leu Pro Thr  
325 330 335

Ala Met Leu Thr Lys Ala Val Tyr Ala Asp Thr Glu Gly Phe Val Ser  
340 345 350

Glu Met Asp Thr Arg Ala Leu Gly Met Ala Val Val Ala Met Gly Gly  
355 360 365

Gly Arg Arg Gln Ala Ser Asp Thr Ile Asp Tyr Ser Val Gly Phe Thr  
370 375 380

6/36

Asp Met Ala Arg Leu Gly Asp Gln Val Asp Gly Gln Arg Pro Leu Ala  
 385                   390                   395                   400

Val Ile His Ala Lys Asp Glu Asn Asn Trp Gln Glu Ala Ala Ala Lys Ala  
405 410 415

Val Lys Ala Ala Ile Lys Leu Ala Asp Lys Ala Pro Glu Ser Thr Pro  
420 425 430

Thr Val Tyr Arg Arg Ile Ser Glu  
435 440

<210> 3  
<211> 720  
<212> DNA  
<213> Escherichia coli

<220>  
<221> CDS  
<222> (1) .. (717)

<400> 3  
atg gct acc cca cac att aat gca gaa atg ggc gat ttc gct gac gta 48  
Met Ala Thr Pro His Ile Asn Ala Glu Met Gly Asp Phe Ala Asp Val  
1 5 10 15

```

gtt ttg atg cca ggc gac ccg ctg cgt gcg aag tat att gct gaa act 96
Val Leu Met Pro Gly Asp Pro Leu Arg Ala Lys Tyr Ile Ala Glu Thr
20          25          30

```

ttc ctt gaa gat gcc cgt gaa gtg aac aac gtt cgc ggt atg ctg ggc 144  
 Phe Leu Glu Asp Ala Arg Glu Val Asn Asn Val Arg Gly Met Leu Gly  
 35 40 45

ttc acc ggt act tac aaa ggc cgc aaa att tcc gta atg ggt cac ggt 192  
 Phe Thr Gly Thr Tyr Lys Gly Arg Lys Ile Ser Val Met Gly His Gly  
 50 55 60

atg ggt atc ccg tcc tgc tcc atc tac acc aaa gaa ctg atc acc gat	240
Met Gly Ile Pro Ser Cys Ser Ile Tyr Thr Lys Glu Leu Ile Thr Asp	
65 70 75 80	

7/36

ttc ggc gtg aag aaa att atc cgc gtg ggt tcc tgt ggc gca gtt ctg	288		
Phe Gly Val Lys Lys Ile Ile Arg Val Gly Ser Cys Gly Ala Val Leu			
85	90	95	
ccg cac gta aaa ctg cgc gac gtc gtt atc ggt atg ggt gcc tgc acc	336		
Pro His Val Lys Leu Arg Asp Val Val Ile Gly Met Gly Ala Cys Thr			
100	105	110	
gat tcc aaa gtt aac cgc atc cgt ttt aaa gac cat gac ttt gcc gct	384		
Asp Ser Lys Val Asn Arg Ile Arg Phe Lys Asp His Asp Phe Ala Ala			
115	120	125	
atc gct gac ttc gac atg gtg cgt aac gca gta gat gca gct aaa gca	432		
Ile Ala Asp Phe Asp Met Val Arg Asn Ala Val Asp Ala Ala Lys Ala			
130	135	140	
ctg ggt att gat gct cgc gtg ggt aac ctg ttc tcc gct gac ctg ttc	480		
Leu Gly Ile Asp Ala Arg Val Gly Asn Leu Phe Ser Ala Asp Leu Phe			
145	150	155	160
tac tct ccg gac ggc gaa atg ttc gac gtg atg gaa aaa tac ggc att	528		
Tyr Ser Pro Asp Gly Glu Met Phe Asp Val Met Glu Lys Tyr Gly Ile			
165	170	175	
ctc ggc gtg gaa atg gaa gcg gct ggt atc tac ggc gtc gct gca gaa	576		
Leu Gly Val Glu Met Glu Ala Ala Gly Ile Tyr Gly Val Ala Ala Glu			
180	185	190	
ttt ggc gcg aaa gcc ctg acc atc tgc acc gta tct gac cac atc cgc	624		
Phe Gly Ala Lys Ala Leu Thr Ile Cys Thr Val Ser Asp His Ile Arg			
195	200	205	
act cac gag cag acc act gcc gct gag cgt cag act acc ttc aac gac	672		
Thr His Glu Gln Thr Thr Ala Ala Glu Arg Gln Thr Thr Phe Asn Asp			
210	215	220	
atg atc aaa atc gca ctg gaa tcc gtt ctg ctg ggc gat aaa gag taa	720		
Met Ile Lys Ile Ala Leu Glu Ser Val Leu Leu Gly Asp Lys Glu			
225	230	235	

&lt;210&gt; 4

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

8/36

&lt;400&gt; 4

Met Ala Thr Pro His Ile Asn Ala Glu Met Gly Asp Phe Ala Asp Val  
1 5 10 15

Val Leu Met Pro Gly Asp Pro Leu Arg Ala Lys Tyr Ile Ala Glu Thr  
20 25 30

Phe Leu Glu Asp Ala Arg Glu Val Asn Asn Val Arg Gly Met Leu Gly  
35 40 45

Phe Thr Gly Thr Tyr Lys Gly Arg Lys Ile Ser Val Met Gly His Gly  
50 55 60

Met Gly Ile Pro Ser Cys Ser Ile Tyr Thr Lys Glu Leu Ile Thr Asp  
65 70 75 80

Phe Gly Val Lys Lys Ile Ile Arg Val Gly Ser Cys Gly Ala Val Leu  
85 90 95

Pro His Val Lys Leu Arg Asp Val Val Ile Gly Met Gly Ala Cys Thr  
100 105 110

Asp Ser Lys Val Asn Arg Ile Arg Phe Lys Asp His Asp Phe Ala Ala  
115 120 125

Ile Ala Asp Phe Asp Met Val Arg Asn Ala Val Asp Ala Ala Lys Ala  
130 135 140

Leu Gly Ile Asp Ala Arg Val Gly Asn Leu Phe Ser Ala Asp Leu Phe  
145 150 155 160

Tyr Ser Pro Asp Gly Glu Met Phe Asp Val Met Glu Lys Tyr Gly Ile  
165 170 175

Leu Gly Val Glu Met Glu Ala Ala Gly Ile Tyr Gly Val Ala Ala Glu  
180 185 190

Phe Gly Ala Lys Ala Leu Thr Ile Cys Thr Val Ser Asp His Ile Arg  
195 200 205

Thr His Glu Gln Thr Thr Ala Ala Glu Arg Gln Thr Thr Phe Asn Asp  
210 215 220

Met Ile Lys Ile Ala Leu Glu Ser Val Leu Leu Gly Asp Lys Glu  
225 230 235

<210> 5  
 <211> 1224  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> CDS  
 <222> (1)..(1221)

<400> 5  
 atg aaa cgt gca ttt att atg gtg ctg gac tca ttc ggc atc ggc gct 48  
 Met Lys Arg Ala Phe Ile Met Val Leu Asp Ser Phe Gly Ile Gly Ala  
 1 5 10 15  
 )  
 aca gaa gat gca gaa cgc ttt ggt gac gtc ggg gct gac acc ctg ggt 96  
 Thr Glu Asp Ala Glu Arg Phe Gly Asp Val Gly Ala Asp Thr Leu Gly  
 20 25 30  
 cat atc gca gaa gct tgt gcc aaa ggc gaa gct gat aac ggt cgt aaa 144  
 His Ile Ala Glu Ala Cys Ala Lys Gly Glu Ala Asp Asn Gly Arg Lys  
 35 40 45  
 ggc ccg ctc aat ctg cca aat ctg acc cgt ctg ggg ctg gcg aaa gca 192  
 Gly Pro Leu Asn Leu Pro Asn Leu Thr Arg Leu Gly Leu Ala Lys Ala  
 50 55 60  
 cac gaa ggt tct acc ggt ttc att ccg gcg gga atg gac ggc aac gct 240  
 His Glu Gly Ser Thr Gly Phe Ile Pro Ala Gly Met Asp Gly Asn Ala  
 65 70 75 80  
 gaa gtt atc ggc gcg tac gca tgg gcg cac gaa atg tca tcc ggt aaa 288  
 Glu Val Ile Gly Ala Tyr Ala Trp Ala His Glu Met Ser Ser Gly Lys  
 85 90 95  
 gat acc ccg tct ggt cac tgg gaa att gcc ggt gtc ccg gtt ctg ttt 336  
 Asp Thr Pro Ser Gly His Trp Glu Ile Ala Gly Val Pro Val Leu Phe  
 100 105 110  
 gag tgg gga tat ttc tcc gat cac gaa aac agc ttc ccg caa gag ctg 384  
 Glu Trp Gly Tyr Phe Ser Asp His Glu Asn Ser Phe Pro Gln Glu Leu  
 115 120 125

10/36

ctg gat aaa ctg gtc gaa cgc gct aat ctg ccg ggt tac ctc ggt aac	432		
Leu Asp Lys Leu Val Glu Arg Ala Asn Leu Pro Gly Tyr Leu Gly Asn			
130	135	140	
tgc cac tct tcc ggt acg gtc att ctg gat caa ctg ggc gaa gag cac	480		
Cys His Ser Ser Gly Thr Val Ile Leu Asp Gln Leu Gly Glu Glu His			
145	150	155	160
atg aaa acc ggc aag ccg att ttc tat acc tcc gct gac tcc gtg ttc	528		
Met Lys Thr Gly Lys Pro Ile Phe Tyr Thr Ser Ala Asp Ser Val Phe			
165	170	175	
cag att gcc tgc cat gaa gaa act ttc ggt ctg gat aaa ctc tac gaa	576		
Gln Ile Ala Cys His Glu Glu Thr Phe Gly Leu Asp Lys Leu Tyr Glu			
180	185	190	
ctg tgc gaa atc gcc cgt gaa gag ctg acc aac ggc ggc tac aat atc	624		
Leu Cys Glu Ile Ala Arg Glu Glu Leu Thr Asn Gly Gly Tyr Asn Ile			
195	200	205	
ggt cgt gtt atc gct cgt ccg ttt atc ggc gac aaa gcc ggt aac ttc	672		
Gly Arg Val Ile Ala Arg Pro Phe Ile Gly Asp Lys Ala Gly Asn Phe			
210	215	220	
cag cgt acc ggt aac cgt cac gac ctg gct gtt gag ccg cca gca ccg	720		
Gln Arg Thr Gly Asn Arg His Asp Leu Ala Val Glu Pro Pro Ala Pro			
225	230	235	240
acc gtg ctg cag aaa ctg gtt gat gaa aaa cac ggc cag gtg gtt tct	768		
Thr Val Leu Gln Lys Leu Val Asp Glu Lys His Gly Gln Val Val Ser			
245	250	255	
gtc ggt aaa att gcg gac atc tac gcc aac tgc ggt atc acc aaa aaa	816		
Val Gly Lys Ile Ala Asp Ile Tyr Ala Asn Cys Gly Ile Thr Lys Lys			
260	265	270	
gtg aaa gcg act ggc ctg gac gcg ctg ttt gac gcc acc atc aaa gag	864		
Val Lys Ala Thr Gly Leu Asp Ala Leu Phe Asp Ala Thr Ile Lys Glu			
275	280	285	
atg aaa gaa gcg ggt gat aac acc atc gtc ttc acc aac ttc gtt gac	912		
Met Lys Glu Ala Gly Asp Asn Thr Ile Val Phe Thr Asn Phe Val Asp			
290	295	300	

11/36

ttc gac tct tcc tgg ggc cac cgt cgc gac gtc gcc ggt tat gcc gcg	960		
Phe Asp Ser Ser Trp Gly His Arg Arg Asp Val Ala Gly Tyr Ala Ala			
305	310	315	320
ggt ctg gaa ctg ttc gac cgc cgt ctg ccg gag ctg atg tct ctg ctg	1008		
Gly Leu Glu Leu Phe Asp Arg Arg Leu Pro Glu Leu Met Ser Leu Leu			
325	330	335	
cgc gat gac gac atc ctg atc ctc acc gct gac cac ggt tgc gat ccg	1056		
Arg Asp Asp Asp Ile Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro			
340	345	350	
acc tgg acc ggt act gac cac acg cgt gaa cac att ccg gta ctg gta	1104		
Thr Trp Thr Gly Thr Asp His Thr Arg Glu His Ile Pro Val Leu Val			
355	360	365	
tat ggc ccg aaa gta aaa ccg ggc tca ctg ggt cat cgt gaa acc ttc	1152		
Tyr Gly Pro Lys Val Lys Pro Gly Ser Leu Gly His Arg Glu Thr Phe			
370	375	380	
gcg gat atc ggc cag act ctg gca aaa tat ttt ggt act tct gat atg	1200		
Ala Asp Ile Gly Gln Thr Leu Ala Lys Tyr Phe Gly Thr Ser Asp Met			
385	390	395	400
gaa tat ggc aaa gcc atg ttc tga	1224		
Glu Tyr Gly Lys Ala Met Phe			
405			
<210> 6			
<211> 407			
<212> PRT			
<213> Escherichia coli			
<400> 6			
Met Lys Arg Ala Phe Ile Met Val Leu Asp Ser Phe Gly Ile Gly Ala			
1	5	10	15
Thr Glu Asp Ala Glu Arg Phe Gly Asp Val Gly Ala Asp Thr Leu Gly			
20	25	30	
His Ile Ala Glu Ala Cys Ala Lys Gly Glu Ala Asp Asn Gly Arg Lys			
35	40	45	

12/36

Gly Pro Leu Asn Leu Pro Asn Leu Thr Arg Leu Gly Leu Ala Lys Ala  
50 55 60

His Glu Gly Ser Thr Gly Phe Ile Pro Ala Gly Met Asp Gly Asn Ala  
65 70 75 80

Glu Val Ile Gly Ala Tyr Ala Trp Ala His Glu Met Ser Ser Gly Lys  
85 90 95

Asp Thr Pro Ser Gly His Trp Glu Ile Ala Gly Val Pro Val Leu Phe  
100 105 110

Glu Trp Gly Tyr Phe Ser Asp His Glu Asn Ser Phe Pro Gln Glu Leu  
115 120 125

Leu Asp Lys Leu Val Glu Arg Ala Asn Leu Pro Gly Tyr Leu Gly Asn  
130 135 140

Cys His Ser Ser Gly Thr Val Ile Leu Asp Gln Leu Gly Glu Glu His  
145 150 155 160

Met Lys Thr Gly Lys Pro Ile Phe Tyr Thr Ser Ala Asp Ser Val Phe  
165 170 175

Gln Ile Ala Cys His Glu Glu Thr Phe Gly Leu Asp Lys Leu Tyr Glu  
180 185 190

Leu Cys Glu Ile Ala Arg Glu Glu Leu Thr Asn Gly Gly Tyr Asn Ile  
195 200 205

Gly Arg Val Ile Ala Arg Pro Phe Ile Gly Asp Lys Ala Gly Asn Phe  
210 215 220

Gln Arg Thr Gly Asn Arg His Asp Leu Ala Val Glu Pro Pro Ala Pro  
225 230 235 240

Thr Val Leu Gln Lys Leu Val Asp Glu Lys His Gly Gln Val Val Ser  
245 250 255

Val Gly Lys Ile Ala Asp Ile Tyr Ala Asn Cys Gly Ile Thr Lys Lys  
260 265 270

Val Lys Ala Thr Gly Leu Asp Ala Leu Phe Asp Ala Thr Ile Lys Glu  
275 280 285

13/36

Met Lys Glu Ala Gly Asp Asn Thr Ile Val Phe Thr Asn Phe Val Asp  
290 295 300

Phe Asp Ser Ser Trp Gly His Arg Arg Asp Val Ala Gly Tyr Ala Ala  
305 310 315 320

Gly Leu Glu Leu Phe Asp Arg Arg Leu Pro Glu Leu Met Ser Leu Leu  
325 330 335

Arg Asp Asp Asp Ile Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro  
340 345 350

Thr Trp Thr Gly Thr Asp His Thr Arg Glu His Ile Pro Val Leu Val  
355 360 365

Tyr Gly Pro Lys Val Lys Pro Gly Ser Leu Gly His Arg Glu Thr Phe  
370 375 380

Ala Asp Ile Gly Gln Thr Leu Ala Lys Tyr Phe Gly Thr Ser Asp Met  
385 390 395 400

Glu Tyr Gly Lys Ala Met Phe  
405

<210> 7

<211> 780

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(777)

<400> 7

atg act gat ctg aaa gca agc agc ctg cgt gca ctg aaa ttg atg gac 48  
Met Thr Asp Leu Lys Ala Ser Ser Leu Arg Ala Leu Lys Leu Met Asp  
1 5 10 15

ctg aac acc ctg aat gac gac acc gac gag aaa gtg atc gcc ctg 96  
Leu Asn Thr Leu Asn Asp Asp Asp Thr Asp Glu Lys Val Ile Ala Leu  
20 25 30

14/36

tgt cat cag gcc aaa act ccg gtc ggc aat acc gcc gct atc tgt atc 144  
 Cys His Gln Ala Lys Thr Pro Val Gly Asn Thr Ala Ala Ile Cys Ile  
 35 40 45

tat cct cgc ttt atc ccg att gct cgc aaa act ctg aaa gag cag ggc 192  
 Tyr Pro Arg Phe Ile Pro Ile Ala Arg Lys Thr Leu Lys Glu Gln Gly  
 50 55 60

acc ccg gaa atc cgt atc gct acg gta acc aac ttc cca cac ggt aac 240  
 Thr Pro Glu Ile Arg Ile Ala Thr Val Thr Asn Phe Pro His Gly Asn  
 65 70 75 80

gac gac atc gac atc gcg ctg gca gaa acc cgt gcg gca atc gcc tac 288  
 Asp Asp Ile Asp Ile Ala Leu Ala Glu Thr Arg Ala Ala Ile Ala Tyr  
 85 90 95

ggt gct gat gaa gtt gac gtt gtg ttc ccg tac cgc gcg ctg atg gcg 336  
 Gly Ala Asp Glu Val Asp Val Val Phe Pro Tyr Arg Ala Leu Met Ala  
 100 105 110

ggt aac gag cag gtt ttt gac ctg gtg aaa gcc tgt aaa gag gct 384  
 Gly Asn Glu Gln Val Gly Phe Asp Leu Val Lys Ala Cys Lys Glu Ala  
 115 120 125

tgc gcg gca gcg aat gta ctg ctg aaa gtg atc atc gaa acc ggc gaa 432  
 Cys Ala Ala Ala Asn Val Leu Leu Lys Val Ile Ile Glu Thr Gly Glu  
 130 135 140

ctg aaa gac gaa gcg ctg atc cgt aaa gcg tct gaa atc tcc atc aaa 480  
 Leu Lys Asp Glu Ala Leu Ile Arg Lys Ala Ser Glu Ile Ser Ile Lys  
 145 150 155 160

gcg ggt gcg gac ttc atc aaa acc tct acc ggt aaa gtg gct gtg aac 528  
 Ala Gly Ala Asp Phe Ile Lys Thr Ser Thr Gly Lys Val Ala Val Asn  
 165 170 175

gcg acg ccg gaa agc gcg cgc atc atg atg gaa gtg atc cgt gat atg 576  
 Ala Thr Pro Glu Ser Ala Arg Ile Met Met Glu Val Ile Arg Asp Met  
 180 185 190

ggc gta gaa aaa acc gtt ggt ttc aaa ccg gcg ggc ggc gtg cgt act 624  
 Gly Val Glu Lys Thr Val Gly Phe Lys Pro Ala Gly Gly Val Arg Thr  
 195 200 205

15/36

gcg gaa gat gcg cag aaa tat ctc gcc att gca gat gaa ctg ttc ggt 672  
 Ala Glu Asp Ala Gln Lys Tyr Leu Ala Ile Ala Asp Glu Leu Phe Gly  
 210 215 220

gct gac tgg gca gat gcg cgt cac tac cgc ttt ggc gct tcc agc ctg 720  
 Ala Asp Trp Ala Asp Ala Arg His Tyr Arg Phe Gly Ala Ser Ser Leu  
 225 230 235 240

ctg gca agc ctg ctg aaa gcg ctg ggt cac ggc gac ggt aag agc gcc 768  
 Leu Ala Ser Leu Leu Lys Ala Leu Gly His Gly Asp Gly Lys Ser Ala  
 245 250 255

agc agc tac taa 780  
 Ser Ser Tyr

<210> 8  
<211> 259  
<212> PRT  
<213> Escherichia coli

<400> 8  
Met Thr Asp Leu Lys Ala Ser Ser Leu Arg Ala Leu Lys Leu Met Asp  
 1 5 10 15

Leu Asn Thr Leu Asn Asp Asp Asp Thr Asp Glu Lys Val Ile Ala Leu  
 20 25 30

Cys His Gln Ala Lys Thr Pro Val Gly Asn Thr Ala Ala Ile Cys Ile  
 35 40 45

Tyr Pro Arg Phe Ile Pro Ile Ala Arg Lys Thr Leu Lys Glu Gln Gly  
 50 55 60

Thr Pro Glu Ile Arg Ile Ala Thr Val Thr Asn Phe Pro His Gly Asn  
 65 70 75 80

Asp Asp Ile Asp Ile Ala Leu Ala Glu Thr Arg Ala Ala Ile Ala Tyr  
 85 90 95

Gly Ala Asp Glu Val Asp Val Val Phe Pro Tyr Arg Ala Leu Met Ala  
 100 105 110

Gly Asn Glu Gln Val Gly Phe Asp Leu Val Lys Ala Cys Lys Glu Ala  
 115 120 125

16/36

Cys Ala Ala Ala Asn Val Leu Leu Lys Val Ile Ile Glu Thr Gly Glu  
130 135 140

Leu Lys Asp Glu Ala Leu Ile Arg Lys Ala Ser Glu Ile Ser Ile Lys  
145 150 155 160

Ala Gly Ala Asp Phe Ile Lys Thr Ser Thr Gly Lys Val Ala Val Asn  
165 170 175

Ala Thr Pro Glu Ser Ala Arg Ile Met Met Glu Val Ile Arg Asp Met  
180 185 190

Gly Val Glu Lys Thr Val Gly Phe Lys Pro Ala Gly Gly Val Arg Thr  
195 200 205

Ala Glu Asp Ala Gln Lys Tyr Leu Ala Ile Ala Asp Glu Leu Phe Gly  
210 215 220

Ala Asp Trp Ala Asp Ala Arg His Tyr Arg Phe Gly Ala Ser Ser Leu  
225 230 235 240

Leu Ala Ser Leu Leu Lys Ala Leu Gly His Gly Asp Gly Lys Ser Ala  
245 250 255

Ser Ser Tyr

<210> 9

<211> 1080

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1077)

<400> 9

atg tct aag att ttt gat ttc gta aaa cct ggc gta atc act ggt gat 48  
Met Ser Lys Ile Phe Asp Phe Val Lys Pro Gly Val Ile Thr Gly Asp

1

5

10

15

17/36

gac gta cag aaa gtt ttc cag gta gca aaa gaa aac aac ttc gca ctg 96  
 Asp Val Gln Lys Val Phe Gln Val Ala Lys Glu Asn Asn Phe Ala Leu  
 20 25 30

cca gca gta aac tgc gtc ggt act gac tcc atc aac gcc gta ctg gaa 144  
 Pro Ala Val Asn Cys Val Gly Thr Asp Ser Ile Asn Ala Val Leu Glu  
 35 40 45

acc gct gct aaa gtt aaa gcg ccg gtt atc gtt cag ttc tcc aac ggt 192  
 Thr Ala Ala Lys Val Lys Ala Pro Val Ile Val Gln Phe Ser Asn Gly  
 50 55 60

ggt gct tcc ttt atc gct ggt aaa ggc gtg aaa tct gac gtt ccg cag 240  
 Gly Ala Ser Phe Ile Ala Gly Lys Gly Val Lys Ser Asp Val Pro Gln  
 65 70 75 80

ggt gct gct atc ctg ggc gcg atc tct ggt gcg cat cac gtt cac cag 288  
 Gly Ala Ala Ile Leu Gly Ala Ile Ser Gly Ala His His Val His Gln  
 85 90 95

atg gct gaa cat tat ggt gtt ccg gtt atc ctg cac act gac cac tgc 336  
 Met Ala Glu His Tyr Gly Val Pro Val Ile Leu His Thr Asp His Cys  
 100 105 110

gcg aag aaa ctg ctg ccg tgg atc gac ggt ctg ttg gac gcg ggt gaa 384  
 Ala Lys Lys Leu Leu Pro Trp Ile Asp Gly Leu Leu Asp Ala Gly Glu  
 115 120 125

aaa cac ttc gca gct acc ggt aag ccg ctg ttc tct cac atg atc 432  
 Lys His Phe Ala Ala Thr Gly Lys Pro Leu Phe Ser Ser His Met Ile  
 130 135 140

gac ctg tct gaa gaa tct ctg caa gag aac atc gaa atc tgc tct aaa 480  
 Asp Leu Ser Glu Glu Ser Leu Gln Glu Asn Ile Glu Ile Cys Ser Lys  
 145 150 155 160

tac ctg gag cgc atg tcc aaa atc ggc atg act ctg gaa atc gaa ctg 528  
 Tyr Leu Glu Arg Met Ser Lys Ile Gly Met Thr Leu Glu Ile Glu Leu  
 165 170 175

ggt tgc acc ggt ggt gaa gaa gac ggc gtg gac aac agc cac atg gac 576  
 Gly Cys Thr Gly Gly Glu Asp Gly Val Asp Asn Ser His Met Asp  
 180 185 190

18/36

gct tct gca ctg tac acc cag ccg gaa gac gtt gat tac gca tac acc 624  
 Ala Ser Ala Leu Tyr Thr Gln Pro Glu Asp Val Asp Tyr Ala Tyr Thr  
 195 200 205

gaa ctg agc aaa atc agc ccg cgt ttc acc atc gca gcg tcc ttc ggt 672  
 Glu Leu Ser Lys Ile Ser Pro Arg Phe Thr Ile Ala Ala Ser Phe Gly  
 210 215 220

aac gta cac ggt gtt tac aag ccg ggt aac gtg gtt ctg act ccg acc 720  
 Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Val Leu Thr Pro Thr  
 225 230 235 240

atc ctg cgt gat tct cag gaa tat gtt tcc aag aaa cac aac ctg ccg 768  
 Ile Leu Arg Asp Ser Gln Glu Tyr Val Ser Lys Lys His Asn Leu Pro  
 245 250 255

cac aac agc ctg aac ttc gta ttc cac ggt ggt tcc ggt tct act gct 816  
 His Asn Ser Leu Asn Phe Val Phe His Gly Gly Ser Gly Ser Thr Ala  
 260 265 270

cag gaa atc aaa gac tcc gta agc tac ggc gta gta aaa atg aac atc 864  
 Gln Glu Ile Lys Asp Ser Val Ser Tyr Gly Val Val Lys Met Asn Ile  
 275 280 285

gat acc gat acc caa tgg gca acc tgg gaa ggc gtt ctg aac tac tac 912  
 Asp Thr Asp Thr Gln Trp Ala Thr Trp Glu Gly Val Leu Asn Tyr Tyr  
 290 295 300

aaa gcg aac gaa gct tat ctg cag ggt cag ctg ggt aac ccg aaa ggc 960  
 Lys Ala Asn Glu Ala Tyr Leu Gln Gly Gln Leu Gly Asn Pro Lys Gly  
 305 310 315 320

gaa gat cag ccg aac aag aaa tac tac gat ccg cgc gta tgg ctg cgt 1008  
 Glu Asp Gln Pro Asn Lys Lys Tyr Tyr Asp Pro Arg Val Trp Leu Arg  
 325 330 335

gcc ggt cag act tcg atg atc gct cgt ctg gag aaa gca ttc cag gaa 1056  
 Ala Gly Gln Thr Ser Met Ile Ala Arg Leu Glu Lys Ala Phe Gln Glu  
 340 345 350

ctg aac gcg atc gac gtt ctg taa 1080  
 Leu Asn Ala Ile Asp Val Leu  
 355

19/36

&lt;210&gt; 10

&lt;211&gt; 359

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 10

Met Ser Lys Ile Phe Asp Phe Val Lys Pro Gly Val Ile Thr Gly Asp  
1 5 10 15

Asp Val Gln Lys Val Phe Gln Val Ala Lys Glu Asn Asn Phe Ala Leu  
20 25 30

Pro Ala Val Asn Cys Val Gly Thr Asp Ser Ile Asn Ala Val Leu Glu  
35 40 45

Thr Ala Ala Lys Val Lys Ala Pro Val Ile Val Gln Phe Ser Asn Gly  
50 55 60

Gly Ala Ser Phe Ile Ala Gly Lys Gly Val Lys Ser Asp Val Pro Gln  
65 70 75 80

Gly Ala Ala Ile Leu Gly Ala Ile Ser Gly Ala His His Val His Gln  
85 90 95

Met Ala Glu His Tyr Gly Val Pro Val Ile Leu His Thr Asp His Cys  
100 105 110

Ala Lys Lys Leu Leu Pro Trp Ile Asp Gly Leu Leu Asp Ala Gly Glu  
115 120 125

Lys His Phe Ala Ala Thr Gly Lys Pro Leu Phe Ser Ser His Met Ile  
130 135 140

Asp Leu Ser Glu Glu Ser Leu Gln Glu Asn Ile Glu Ile Cys Ser Lys  
145 150 155 160

Tyr Leu Glu Arg Met Ser Lys Ile Gly Met Thr Leu Glu Ile Glu Leu  
165 170 175

Gly Cys Thr Gly Gly Glu Asp Gly Val Asp Asn Ser His Met Asp  
180 185 190

Ala Ser Ala Leu Tyr Thr Gln Pro Glu Asp Val Asp Tyr Ala Tyr Thr  
195 200 205

20/36

Glu Leu Ser Lys Ile Ser Pro Arg Phe Thr Ile Ala Ala Ser Phe Gly  
 210 215 220

Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Val Leu Thr Pro Thr  
 225 230 235 240

Ile Leu Arg Asp Ser Gln Glu Tyr Val Ser Lys Lys His Asn Leu Pro  
 245 250 255

His Asn Ser Leu Asn Phe Val Phe His Gly Gly Ser Gly Ser Thr Ala  
 260 265 270

Gln Glu Ile Lys Asp Ser Val Ser Tyr Gly Val Val Lys Met Asn Ile  
 275 280 285

Asp Thr Asp Thr Gln Trp Ala Thr Trp Glu Gly Val Leu Asn Tyr Tyr  
 290 295 300

Lys Ala Asn Glu Ala Tyr Leu Gln Gly Gln Leu Gly Asn Pro Lys Gly  
 305 310 315 320

Glu Asp Gln Pro Asn Lys Lys Tyr Tyr Asp Pro Arg Val Trp Leu Arg  
 325 330 335

Ala Gly Gln Thr Ser Met Ile Ala Arg Leu Glu Lys Ala Phe Gln Glu  
 340 345 350

Leu Asn Ala Ile Asp Val Leu  
 355

<210> 11  
 <211> 921  
 <212> DNA  
 <213> *Salmonella typhi*

<220>  
 <221> CDS  
 <222> (1)..(918)

<400> 11  
 atg gat atc gcg gtt att ggc tct aac atg gtg gac ctt atc acc tac 48  
 Met Asp Ile Ala Val Ile Gly Ser Asn Met Val Asp Leu Ile Thr Tyr  
 1 5 10 15

21/36

acc aac cag atg ccc aaa gaa ggg gaa act ctg gaa gcg ccg gcg ttt	96		
Thr Asn Gln Met Pro Lys Glu Gly Glu Thr Leu Glu Ala Pro Ala Phe			
20	25	30	
aaa atc ggc tgc ggc gga aaa ggg gcg aac cag gcc gtg gcg gcc gct	144		
Lys Ile Gly Cys Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Ala			
35	40	45	
aag ctc aat tca aaa gta ttg atg ttg acc aaa gtg ggc gac gat att	192		
Lys Leu Asn Ser Lys Val Leu Met Leu Thr Lys Val Gly Asp Asp Ile			
50	55	60	
ttt gcc gac aac acc att cgt aat ctc gaa tcc tgg ggg atc aat acg	240		
Phe Ala Asp Asn Thr Ile Arg Asn Leu Glu Ser Trp Gly Ile Asn Thr			
65	70	75	80
acg tat gta gaa aaa gta ccg tgt acc agc agc ggc gta gcg ccg att	288		
Thr Tyr Val Glu Lys Val Pro Cys Thr Ser Ser Gly Val Ala Pro Ile			
85	90	95	
ttc gtc aac gcc aac tcc agc aac agc att ctg atc atc aaa ggc gct	336		
Phe Val Asn Ala Asn Ser Ser Asn Ser Ile Leu Ile Ile Lys Gly Ala			
100	105	110	
aac aag ttt ctc tcg ccg gaa gat atc gat cgc gcg gaa gat tta	384		
Asn Lys Phe Leu Ser Pro Glu Asp Ile Asp Arg Ala Ala Glu Asp Leu			
115	120	125	
aaa aaa tgc cag ctt att gtt ctg caa ctg gaa gtt cag ctt gaa acg	432		
Lys Lys Cys Gln Leu Ile Val Leu Gln Leu Glu Val Gln Leu Glu Thr			
130	135	140	
gtt tat cac gca ata gaa ttt ggc aag aaa cac ggg att gaa gtg tta	480		
Val Tyr His Ala Ile Glu Phe Gly Lys Lys His Gly Ile Glu Val Leu			
145	150	155	160
tta aac cct gcg cca gca tta cgg gaa tta gat atg tct tat gcc tgt	528		
Leu Asn Pro Ala Pro Ala Leu Arg Glu Leu Asp Met Ser Tyr Ala Cys			
165	170	175	
aaa tgc gat ttc ttt gta cct aat gaa acc gag ctg gaa ata tta acc	576		
Lys Cys Asp Phe Phe Val Pro Asn Glu Thr Glu Leu Glu Ile Leu Thr			
180	185	190	

22/36

ggt atg cca gtg gat acc tat gac cat att cgc gca gcg gca cgt tcg 624  
 Gly Met Pro Val Asp Thr Tyr Asp His Ile Arg Ala Ala Ala Arg Ser  
 195 200 205

ctg gta gat aaa ggg ctg aac aat att att gtc acc atg ggc gag aaa 672  
 Leu Val Asp Lys Gly Leu Asn Asn Ile Ile Val Thr Met Gly Glu Lys  
 210 215 220

ggc gcg ctg tgg atg acg cgt gac cag gaa gtc cat gtt ccg gcg ttt 720  
 Gly Ala Leu Trp Met Thr Arg Asp Gln Glu Val His Val Pro Ala Phe  
 225 230 235 240

aga gtg aac gct gtt gat acc agc ggc gcg ggc gat gcc ttt atc ggc 768  
 Arg Val Asn Ala Val Asp Thr Ser Gly Ala Gly Asp Ala Phe Ile Gly  
 245 250 255

tgt ttc gcg cat tac tac gtc cag agc ggg gat gtg gaa gcc gcc atg 816  
 Cys Phe Ala His Tyr Tyr Val Gln Ser Gly Asp Val Glu Ala Ala Met  
 260 265 270

aaa aaa gcc gtc ctc ttt gcc gct ttc agc gtc acc ggg aaa ggc acc 864  
 Lys Lys Ala Val Leu Phe Ala Ala Phe Ser Val Thr Gly Lys Gly Thr  
 275 280 285

caa tcc tct tat cca agc att gag caa ttt aat gag tat ctt tcg ttg 912  
 Gln Ser Ser Tyr Pro Ser Ile Glu Gln Phe Asn Glu Tyr Leu Ser Leu  
 290 295 300

aac gaa taa 921  
 Asn Glu  
 305

<210> 12  
 <211> 306  
 <212> PRT  
 <213> *Salmonella typhi*

<400> 12  
 Met Asp Ile Ala Val Ile Gly Ser Asn Met Val Asp Leu Ile Thr Tyr  
 1 5 10 15

Thr Asn Gln Met Pro Lys Glu Gly Glu Thr Leu Glu Ala Pro Ala Phe  
 20 25 30

23/36

Lys Ile Gly Cys Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Ala  
35 40 45

Lys Leu Asn Ser Lys Val Leu Met Leu Thr Lys Val Gly Asp Asp Ile  
50 55 60

Phe Ala Asp Asn Thr Ile Arg Asn Leu Glu Ser Trp Gly Ile Asn Thr  
65 70 75 80

Thr Tyr Val Glu Lys Val Pro Cys Thr Ser Ser Gly Val Ala Pro Ile  
85 90 95

Phe Val Asn Ala Asn Ser Ser Asn Ser Ile Leu Ile Ile Lys Gly Ala  
100 105 110

Asn Lys Phe Leu Ser Pro Glu Asp Ile Asp Arg Ala Ala Glu Asp Leu  
115 120 125

Lys Lys Cys Gln Leu Ile Val Leu Gln Leu Glu Val Gln Leu Glu Thr  
130 135 140

Val Tyr His Ala Ile Glu Phe Gly Lys His Gly Ile Glu Val Leu  
145 150 155 160

Leu Asn Pro Ala Pro Ala Leu Arg Glu Leu Asp Met Ser Tyr Ala Cys  
165 170 175

Lys Cys Asp Phe Phe Val Pro Asn Glu Thr Glu Leu Glu Ile Leu Thr  
180 185 190

Gly Met Pro Val Asp Thr Tyr Asp His Ile Arg Ala Ala Ala Arg Ser  
195 200 205

Leu Val Asp Lys Gly Leu Asn Asn Ile Ile Val Thr Met Gly Glu Lys  
210 215 220

Gly Ala Leu Trp Met Thr Arg Asp Gln Glu Val His Val Pro Ala Phe  
225 230 235 240

Arg Val Asn Ala Val Asp Thr Ser Gly Ala Gly Asp Ala Phe Ile Gly  
245 250 255

Cys Phe Ala His Tyr Tyr Val Gln Ser Gly Asp Val Glu Ala Ala Met  
260 265 270

24/36

Lys Lys Ala Val Leu Phe Ala Ala Phe Ser Val Thr Gly Lys Gly Thr  
 275 280 285

Gln Ser Ser Tyr Pro Ser Ile Glu Gln Phe Asn Glu Tyr Leu Ser Leu  
 290 295 300

Asn Glu  
 305

&lt;210&gt; 13

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Lactobacillus leichmannii

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (10) .. (480)

&lt;400&gt; 13

gtataactaa atg cca aaa aag acg atc tac ttc ggt gcc ggc tgg ttc act 51  
 Met Pro Lys Lys Thr Ile Tyr Phe Gly Ala Gly Trp Phe Thr  
 1 5 10

gac cgc caa aac aaa gcc tac aag gaa gcc atg gaa gcc ctc aag gaa 99  
 Asp Arg Gln Asn Lys Ala Tyr Lys Glu Ala Met Glu Ala Leu Lys Glu  
 15 20 25 30

aac cca acg att gac ctg gaa aac acg tac gtt ccc ctg gac aac cag 147  
 Asn Pro Thr Ile Asp Leu Glu Asn Ser Tyr Val Pro Leu Asp Asn Gln  
 35 40 45

tac aag ggt atc cgg gtt gat gaa cac ccg gaa tac ctg cat gac aag 195  
 Tyr Lys Gly Ile Arg Val Asp Glu His Pro Glu Tyr Leu His Asp Lys  
 50 55 60

gtt tgg gct acg gcc acc tac aac aac gac ttg aac ggg atc aag acc 243  
 Val Trp Ala Thr Ala Thr Tyr Asn Asn Asp Leu Asn Gly Ile Lys Thr  
 65 70 75

aac gac atc atg ctg ggt gtc tac atc cct gac gaa gaa gac gtc ggc 291  
 Asn Asp Ile Met Leu Gly Val Tyr Ile Pro Asp Glu Glu Asp Val Gly  
 80 85 90

25/36

ctg ggc atg gaa ctg ggt tac gcc ttg agc caa ggc aag tac gtc ctt 339  
 Leu Gly Met Glu Leu Gly Tyr Ala Leu Ser Gln Gly Lys Tyr Val Leu  
 95 100 105 110

ttg gtc atc ccg gac gaa gac tac ggc aag ccg atc aac ctc atg agc 387  
 Leu Val Ile Pro Asp Glu Asp Tyr Gly Lys Pro Ile Asn Leu Met Ser  
 115 120 125

tgg ggc gtc agc gac aac gtg atc aag atg agc cag ctg aag gac ttc 435  
 Trp Gly Val Ser Asp Asn Val Ile Lys Met Ser Gln Leu Lys Asp Phe  
 130 135 140

aac ttc aac aag ccg cgc ttc gac ttc tac gaa ggt gcc gta tac taa 483  
 Asn Phe Asn Lys Pro Arg Phe Asp Phe Tyr Glu Gly Ala Val Tyr  
 145 150 155

&lt;210&gt; 14

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Lactobacillus leichmannii

&lt;400&gt; 14

Met Pro Lys Lys Thr Ile Tyr Phe Gly Ala Gly Trp Phe Thr Asp Arg  
 1 5 10 15

Gln Asn Lys Ala Tyr Lys Glu Ala Met Glu Ala Leu Lys Glu Asn Pro  
 20 25 30

Thr Ile Asp Leu Glu Asn Ser Tyr Val Pro Leu Asp Asn Gln Tyr Lys  
 35 40 45

Gly Ile Arg Val Asp Glu His Pro Glu Tyr Leu His Asp Lys Val Trp  
 50 55 60

Ala Thr Ala Thr Tyr Asn Asn Asp Leu Asn Gly Ile Lys Thr Asn Asp  
 65 70 75 80

Ile Met Leu Gly Val Tyr Ile Pro Asp Glu Glu Asp Val Gly Leu Gly  
 85 90 95

Met Glu Leu Gly Tyr Ala Leu Ser Gln Gly Lys Tyr Val Leu Leu Val  
 100 105 110

26/36

Ile Pro Asp Glu Asp Tyr Gly Lys Pro Ile Asn Leu Met Ser Trp Gly  
 115 120 125

Val Ser Asp Asn Val Ile Lys Met Ser Gln Leu Lys Asp Phe Asn Phe  
 130 135 140

Asn Lys Pro Arg Phe Asp Phe Tyr Glu Gly Ala Val Tyr  
 145 150 155

<210> 15

<211> 720

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(717)

<400> 15

atg gct acc cca cac att aat gca gaa atg ggc gat ttc gct gac gta 48  
 Met Ala Thr Pro His Ile Asn Ala Glu Met Gly Asp Phe Ala Asp Val  
 1 5 10 15

gtt ttg atg cca ggc gac ccg ctg cgt gcg aag tat att gct gaa act 96  
 Val Leu Met Pro Gly Asp Pro Leu Arg Ala Lys Tyr Ile Ala Glu Thr  
 20 25 30

ttc ctt gaa gat gcc cgt gaa gtg aac aac gtt cgc ggt atg ctg ggc 144  
 Phe Leu Glu Asp Ala Arg Glu Val Asn Asn Val Arg Gly Met Leu Gly  
 35 40 45

ttc acc ggt act tac aaa ggc cgc aaa att tcc gta atg ggt cac ggt 192  
 Phe Thr Gly Thr Tyr Lys Gly Arg Lys Ile Ser Val Met Gly His Gly  
 50 55 60

atg ggt atc ccg tcc tgc tcc atc tac acc aaa gaa ctg atc acc gat 240  
 Met Gly Ile Pro Ser Cys Ser Ile Tyr Thr Lys Glu Leu Ile Thr Asp  
 65 70 75 80

ttc ggc gtg aag aaa att atc cgc gtg ggt tcc tgt ggc gca gtt ctg 288  
 Phe Gly Val Lys Lys Ile Ile Arg Val Gly Ser Cys Gly Ala Val Leu  
 85 90 95

27/36

ccg cac gta aaa ctg cgc gac gtc gtt atc ggt atg ggt acc tgc acc 336  
 Pro His Val Lys Leu Arg Asp Val Val Ile Gly Met Gly Thr Cys Thr  
 100 105 110

gat tcc aaa gtt aac cgc atc cgt ttt aaa gac cat gac ttt gcc gct 384  
 Asp Ser Lys Val Asn Arg Ile Arg Phe Lys Asp His Asp Phe Ala Ala  
 115 120 125

atc gct gac ttc gac atg gtg cgt aac gca gta gat gca gct aaa gca 432  
 Ile Ala Asp Phe Asp Met Val Arg Asn Ala Val Asp Ala Ala Lys Ala  
 130 135 140

ctg ggt att gat gct cgc gtg ggt aac ctg ttc tcc gct gac ctg ttc 480  
 Leu Gly Ile Asp Ala Arg Val Gly Asn Leu Phe Ser Ala Asp Leu Phe  
 145 150 155 160

tac tct ccg gac ggc gaa atg ttc gac gtg atg gaa aaa tac ggc att 528  
 Tyr Ser Pro Asp Gly Glu Met Phe Asp Val Met Glu Lys Tyr Gly Ile  
 165 170 175

ctc ggc gtg gaa atg gaa gcg gct ggt atc tac ggc gtc gct gca gaa 576  
 Leu Gly Val Glu Met Glu Ala Ala Gly Ile Tyr Gly Val Ala Ala Glu  
 180 185 190

ttt ggc gcg aaa gcc ctg acc atc tgc acc gta tct gac cac atc cgc 624  
 Phe Gly Ala Lys Ala Leu Thr Ile Cys Thr Val Ser Asp His Ile Arg  
 195 200 205

act cac gag cag acc act gcc gct gag cgt act acc ttc aac aac 672  
 Thr His Glu Gln Thr Ala Ala Glu Arg Gln Thr Phe Asn Asn  
 210 215 220

atg atc aaa atc gca ctg gaa tcc gtt ctg ctg ggc gat aaa gag taa 720  
 Met Ile Lys Ile Ala Leu Glu Ser Val Leu Leu Gly Asp Lys Glu  
 225 230 235

<210> 16  
 <211> 239  
 <212> PRT  
 <213> Escherichia coli

<400> 16  
 Met Ala Thr Pro His Ile Asn Ala Glu Met Gly Asp Phe Ala Asp Val  
 1 5 10 15

28/36

Val Leu Met Pro Gly Asp Pro Leu Arg Ala Lys Tyr Ile Ala Glu Thr  
20 25 30

Phe Leu Glu Asp Ala Arg Glu Val Asn Asn Val Arg Gly Met Leu Gly  
35 40 45

Phe Thr Gly Thr Tyr Lys Gly Arg Lys Ile Ser Val Met Gly His Gly  
50 55 60

Met Gly Ile Pro Ser Cys Ser Ile Tyr Thr Lys Glu Leu Ile Thr Asp  
65 70 75 80

Phe Gly Val Lys Lys Ile Ile Arg Val Gly Ser Cys Gly Ala Val Leu  
85 90 95

Pro His Val Lys Leu Arg Asp Val Val Ile Gly Met Gly Thr Cys Thr  
100 105 110

Asp Ser Lys Val Asn Arg Ile Arg Phe Lys Asp His Asp Phe Ala Ala  
115 120 125

Ile Ala Asp Phe Asp Met Val Arg Asn Ala Val Asp Ala Ala Lys Ala  
130 135 140

Leu Gly Ile Asp Ala Arg Val Gly Asn Leu Phe Ser Ala Asp Leu Phe  
145 150 155 160

Tyr Ser Pro Asp Gly Glu Met Phe Asp Val Met Glu Lys Tyr Gly Ile  
165 170 175

Leu Gly Val Glu Met Glu Ala Ala Gly Ile Tyr Gly Val Ala Ala Glu  
180 185 190

Phe Gly Ala Lys Ala Leu Thr Ile Cys Thr Val Ser Asp His Ile Arg  
195 200 205

Thr His Glu Gln Thr Thr Ala Ala Glu Arg Gln Thr Thr Phe Asn Asn  
210 215 220

Met Ile Lys Ile Ala Leu Glu Ser Val Leu Leu Gly Asp Lys Glu  
225 230 235

29/36

&lt;211&gt; 1224

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1221)

&lt;400&gt; 17

atg aaa cgt gca ttt att atg gtg ctg gac tca ttc ggc atc ggc gct 48  
 Met Lys Arg Ala Phe Ile Met Val Leu Asp Ser Phe Gly Ile Gly Ala  
 1 5 10 15

aca gaa gat gca gaa cgc ttt ggt gac gtc ggg gct gac acc ctg ggt 96  
 Thr Glu Asp Ala Glu Arg Phe Gly Asp Val Gly Ala Asp Thr Leu Gly  
 20 25 30

cat atc gca gaa gct tgt gcc aaa ggc gaa gct gat aac ggt cgt aaa 144  
 His Ile Ala Glu Ala Cys Ala Lys Gly Glu Ala Asp Asn Gly Arg Lys  
 35 40 45

ggc ccg ctc aat ctg cca aat ctg acc cgt ctg ggg ctg gcg aaa gca 192  
 Gly Pro Leu Asn Leu Pro Asn Leu Thr Arg Leu Gly Leu Ala Lys Ala  
 50 55 60

cac gaa ggt tct acc ggt ttc att ccg gcg gga atg gac ggc aac gct 240  
 His Glu Gly Ser Thr Gly Phe Ile Pro Ala Gly Met Asp Gly Asn Ala  
 65 70 75 80

gaa gtt atc ggc gcg tac gca tgg gcg cac gaa atg tca tcc ggt aaa 288  
 Glu Val Ile Gly Ala Tyr Ala Trp Ala His Glu Met Ser Ser Gly Lys  
 85 90 95

gat acc ccg tct ggt cac tgg gaa att gcc ggc gtc ccg gtt ctg ttt 336  
 Asp Thr Pro Ser Gly His Trp Glu Ile Ala Gly Val Pro Val Leu Phe  
 100 105 110

gag tgg gga tat ttc tcc gat cac gaa aac agc ttc ccg caa gag ctg 384  
 Glu Trp Gly Tyr Phe Ser Asp His Glu Asn Ser Phe Pro Gln Glu Leu  
 115 120 125

ctg gat aaa ctg gtc gaa cgc gct aat ctg ccg ggt tac ctc ggt aac 432  
 Leu Asp Lys Leu Val Glu Arg Ala Asn Leu Pro Gly Tyr Leu Gly Asn  
 130 135 140

30/36

tgc cac tct tcc ggt acg gtc att ctg gat caa ctg ggc gaa gag cac	480		
Cys His Ser Ser Gly Thr Val Ile Leu Asp Gln Leu Gly Glu Glu His			
145	150	155	160
atg aaa acc ggc aag ccg att ttc tat acc tcc gct gac tcc gtg ttc	528		
Met Lys Thr Gly Lys Pro Ile Phe Tyr Thr Ser Ala Asp Ser Val Phe			
165	170	175	
cag att gcc tgc cat gaa gaa act ttc ggt ctg gat aaa ctc tac gaa	576		
Gln Ile Ala Cys His Glu Glu Thr Phe Gly Leu Asp Lys Leu Tyr Glu			
180	185	190	
ctg tgc gaa atc gcc cgt gaa gag ctg acc aac ggc ggc tac aat atc	624		
Leu Cys Glu Ile Ala Arg Glu Glu Leu Thr Asn Gly Gly Tyr Asn Ile			
195	200	205	
ggt cgt gtt atc gct cgt ccg ttt atc ggc gac aaa gcc ggt aac ttc	672		
Gly Arg Val Ile Ala Arg Pro Phe Ile Gly Asp Lys Ala Gly Asn Phe			
210	215	220	
caa cgt acc ggt aac cgt cac gac ctg gct gtt gag ccg cca gca ccg	720		
Gln Arg Thr Gly Asn Arg His Asp Leu Ala Val Glu Pro Pro Ala Pro			
225	230	235	240
acc gtg ctg cag aaa ctg gtt gat gaa aaa cac ggc cag gtg gtt tct	768		
Thr Val Leu Gln Lys Leu Val Asp Glu Lys His Gly Gln Val Val Ser			
245	250	255	
gtc ggt aaa att gcg gac atc tac gac gcc aac tgc ggt atc acc aaa aaa	816		
Val Gly Lys Ile Ala Asp Ile Tyr Ala Asn Cys Gly Ile Thr Lys Lys			
260	265	270	
gtg aaa gcg act ggc ctg gac gcg ctg ttt gac acc acc atc aaa gag	864		
Val Lys Ala Thr Gly Leu Asp Ala Leu Phe Asp Thr Thr Ile Lys Glu			
275	280	285	
atg aaa gaa gcg ggt gat aac acc atc gtc ttc acc aac ttc gtt gac	912		
Met Lys Glu Ala Gly Asp Asn Thr Ile Val Phe Thr Asn Phe Val Asp			
290	295	300	
ttc gac tct tcc tgg ggc cac cgt cgc gac gtc gcc ggt tat gcc gcg	960		
Phe Asp Ser Ser Trp Gly His Arg Arg Asp Val Ala Gly Tyr Ala Ala			
305	310	315	320

31/36

gg t ctg gaa ctg ttc gac cgc cgt ctg ccg gag ctg atg tct ctg ctg 1008  
 Gly Leu Glu Leu Phe Asp Arg Arg Leu Pro Glu Leu Met Ser Leu Leu  
 325 330 335

cgc gat gac gac atc ctg atc ctc acc gct gac cac ggt tgc gat ccg 1056  
 Arg Asp Asp Asp Ile Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro  
 340 345 350

acc tgg acc ggt act gac cac acg cgt gaa cac att ccg gta ctg gta 1104  
 Thr Trp Thr Gly Thr Asp His Thr Arg Glu His Ile Pro Val Leu Val  
 355 360 365

tat ggc ccg aaa gta aaa ccg ggc tca ctg ggt cat cgt gaa acc ttc 1152  
 Tyr Gly Pro Lys Val Lys Pro Gly Ser Leu Gly His Arg Glu Thr Phe  
 370 375 380

gcg gat atc ggc cag act ctg gca aaa tat ttt ggt act tct gat atg 1200  
 Ala Asp Ile Gly Gln Thr Leu Ala Lys Tyr Phe Gly Thr Ser Asp Met  
 385 390 395 400

gaa tat ggc aaa gcc atg ttc tga 1224  
 Glu Tyr Gly Lys Ala Met Phe  
 405

<210> 18  
<211> 407  
<212> PRT  
<213> Escherichia coli

<400> 18  
Met Lys Arg Ala Phe Ile Met Val Leu Asp Ser Phe Gly Ile Gly Ala  
 1 5 10 15

Thr Glu Asp Ala Glu Arg Phe Gly Asp Val Gly Ala Asp Thr Leu Gly  
 20 25 30

His Ile Ala Glu Ala Cys Ala Lys Gly Glu Ala Asp Asn Gly Arg Lys  
 35 40 45

Gly Pro Leu Asn Leu Pro Asn Leu Thr Arg Leu Gly Leu Ala Lys Ala  
 50 55 60

His Glu Gly Ser Thr Gly Phe Ile Pro Ala Gly Met Asp Gly Asn Ala  
 65 70 75 80

32/36

Glu Val Ile Gly Ala Tyr Ala Trp Ala His Glu Met Ser Ser Gly Lys  
85 90 95

Asp Thr Pro Ser Gly His Trp Glu Ile Ala Gly Val Pro Val Leu Phe  
100 105 110

Glu Trp Gly Tyr Phe Ser Asp His Glu Asn Ser Phe Pro Gln Glu Leu  
115 120 125

Leu Asp Lys Leu Val Glu Arg Ala Asn Leu Pro Gly Tyr Leu Gly Asn  
130 135 140

Cys His Ser Ser Gly Thr Val Ile Leu Asp Gln Leu Gly Glu Glu His  
145 150 155 160

Met Lys Thr Gly Lys Pro Ile Phe Tyr Thr Ser Ala Asp Ser Val Phe  
165 170 175

Gln Ile Ala Cys His Glu Glu Thr Phe Gly Leu Asp Lys Leu Tyr Glu  
180 185 190

Leu Cys Glu Ile Ala Arg Glu Glu Leu Thr Asn Gly Gly Tyr Asn Ile  
195 200 205

Gly Arg Val Ile Ala Arg Pro Phe Ile Gly Asp Lys Ala Gly Asn Phe  
210 215 220

Gln Arg Thr Gly Asn Arg His Asp Leu Ala Val Glu Pro Pro Ala Pro  
225 230 235 240

Thr Val Leu Gln Lys Leu Val Asp Glu Lys His Gly Gln Val Val Ser  
245 250 255

Val Gly Lys Ile Ala Asp Ile Tyr Ala Asn Cys Gly Ile Thr Lys Lys  
260 265 270

Val Lys Ala Thr Gly Leu Asp Ala Leu Phe Asp Thr Thr Ile Lys Glu  
275 280 285

Met Lys Glu Ala Gly Asp Asn Thr Ile Val Phe Thr Asn Phe Val Asp  
290 295 300

Phe Asp Ser Ser Trp Gly His Arg Arg Asp Val Ala Gly Tyr Ala Ala  
305 310 315 320

33/36

Gly Leu Glu Leu Phe Asp Arg Arg Leu Pro Glu Leu Met Ser Leu Leu  
 325 330 335

Arg Asp Asp Asp Ile Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro  
 340 345 350

Thr Trp Thr Gly Thr Asp His Thr Arg Glu His Ile Pro Val Leu Val  
 355 360 365

Tyr Gly Pro Lys Val Lys Pro Gly Ser Leu Gly His Arg Glu Thr Phe  
 370 375 380

Ala Asp Ile Gly Gln Thr Leu Ala Lys Tyr Phe Gly Thr Ser Asp Met  
 385 390 395 400

Glu Tyr Gly Lys Ala Met Phe  
 405

&lt;210&gt; 19

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(777)

&lt;400&gt; 19

atg act gat ctg aaa gca agc agc ctg cgt gca ctg aaa ttg atg gac 48  
 Met Thr Asp Leu Lys Ala Ser Ser Leu Arg Ala Leu Lys Leu Met Asp  
 1 5 10 15

ctg aac acc ctg aat gac gac acc gac gag aaa gtg atc gcc ctg 96  
 Leu Asn Thr Leu Asn Asp Asp Asp Thr Asp Glu Lys Val Ile Ala Leu  
 20 25 30

tgt cat cag gcc aaa act ccg gtc ggc aat acc gcc gct atc tgt atc 144  
 Cys His Gln Ala Lys Thr Pro Val Gly Asn Thr Ala Ala Ile Cys Ile  
 35 40 45

tat cct cgc ttt atc ccg att gct cgc aaa act ctg aaa gag cag ggc 192  
 Tyr Pro Arg Phe Ile Pro Ile Ala Arg Lys Thr Leu Lys Glu Gln Gly  
 50 55 60

34/36

acc ccg gaa atc cgt atc gct acg gta acc aac ttc cca cac ggt aac 240  
 Thr Pro Glu Ile Arg Ile Ala Thr Val Thr Asn Phe Pro His Gly Asn  
 65 70 75 80

gac gac atc gac atc gcg ctg gca gaa acc cgt gcg gca atc gcc tac 288  
 Asp Asp Ile Asp Ile Ala Leu Ala Glu Thr Arg Ala Ala Ile Ala Tyr  
 85 90 95

ggt gct gat gaa gtt gac gtt gtg ttc ccg tac cgc gcg ctg atg gcg 336  
 Gly Ala Asp Glu Val Asp Val Val Phe Pro Tyr Arg Ala Leu Met Ala  
 100 105 110

ggt aac gag cag gtt ggt ttt gac ctg gtg aaa gcc tgt aaa gag gct 384  
 Gly Asn Glu Gln Val Gly Phe Asp Leu Val Lys Ala Cys Lys Glu Ala  
 115 120 125

tgc gcg gca gcg aat gta ctg ctg aaa gtg atc atc gaa acc ggc gaa 432  
 Cys Ala Ala Ala Asn Val Leu Leu Lys Val Ile Ile Glu Thr Gly Glu  
 130 135 140

ctg aaa gac gaa gcg ctg atc cgt aaa gcg tct gaa atc tcc atc aaa 480  
 Leu Lys Asp Glu Ala Leu Ile Arg Lys Ala Ser Glu Ile Ser Ile Lys  
 145 150 155 160

gcg ggt gtg gac ttc atc aaa acc tct acc ggt aaa gtg gct gtg aac 528  
 Ala Gly Val Asp Phe Ile Lys Thr Ser Thr Gly Lys Val Ala Val Asn  
 165 170 175

gcg acg ccg gaa agc gcg cgc atc atg atg gaa gtg atc cgt gat atg 576  
 Ala Thr Pro Glu Ser Ala Arg Ile Met Met Glu Val Ile Arg Asp Met  
 180 185 190

ggc gta gaa aaa acc gtt ggt ttc aaa ccg gcg ggc ggc gtg cgt act 624  
 Gly Val Glu Lys Thr Val Gly Phe Lys Pro Ala Gly Gly Val Arg Thr  
 195 200 205

gcg gaa gat gcg cag aaa tat ctc gcc att gca gat gaa ctg ttc ggt 672  
 Ala Glu Asp Ala Gln Lys Tyr Leu Ala Ile Ala Asp Glu Leu Phe Gly  
 210 215 220

gct gac tgg gca gat gcg cgt cac tac cgc ttt ggc gct tcc agc ctg 720  
 Ala Asp Trp Ala Asp Ala Arg His Tyr Arg Phe Gly Ala Ser Ser Leu  
 225 230 235 240

35/36

ctg gca agc ctg ctg aaa gcg ctg ggt cac ggc gac ggt aag agc gcc 768  
 Leu Ala Ser Leu Leu Lys Ala Leu Gly His Gly Asp Gly Lys Ser Ala  
 245 250 255

agc agc tac taa 780  
 Ser Ser Tyr

<210> 20  
 <211> 259  
 <212> PRT  
 <213> Escherichia coli

<400> 20  
 Met Thr Asp Leu Lys Ala Ser Ser Leu Arg Ala Leu Lys Leu Met Asp  
 1 5 10 15

Leu Asn Thr Leu Asn Asp Asp Asp Thr Asp Glu Lys Val Ile Ala Leu  
 20 25 30

Cys His Gln Ala Lys Thr Pro Val Gly Asn Thr Ala Ala Ile Cys Ile  
 35 40 45

Tyr Pro Arg Phe Ile Pro Ile Ala Arg Lys Thr Leu Lys Glu Gln Gly  
 50 55 60

Thr Pro Glu Ile Arg Ile Ala Thr Val Thr Asn Phe Pro His Gly Asn  
 65 70 75 80

Asp Asp Ile Asp Ile Ala Leu Ala Glu Thr Arg Ala Ala Ile Ala Tyr  
 85 90 95

Gly Ala Asp Glu Val Asp Val Val Phe Pro Tyr Arg Ala Leu Met Ala  
 100 105 110

Gly Asn Glu Gln Val Gly Phe Asp Leu Val Lys Ala Cys Lys Glu Ala  
 115 120 125

Cys Ala Ala Ala Asn Val Leu Leu Lys Val Ile Ile Glu Thr Gly Glu  
 130 135 140

Leu Lys Asp Glu Ala Leu Ile Arg Lys Ala Ser Glu Ile Ser Ile Lys  
 145 150 155 160

36/36

Ala Gly Val Asp Phe Ile Lys Thr Ser Thr Gly Lys Val Ala Val Asn  
165 170 175

Ala Thr Pro Glu Ser Ala Arg Ile Met Met Glu Val Ile Arg Asp Met  
180 185 190

Gly Val Glu Lys Thr Val Gly Phe Lys Pro Ala Gly Gly Val Arg Thr  
195 200 205

Ala Glu Asp Ala Gln Lys Tyr Leu Ala Ile Ala Asp Glu Leu Phe Gly  
210 215 220

Ala Asp Trp Ala Asp Ala Arg His Tyr Arg Phe Gly Ala Ser Ser Leu  
225 230 235 240

Leu Ala Ser Leu Leu Lys Ala Leu Gly His Gly Asp Gly Lys Ser Ala  
245 250 255

Ser Ser Tyr